CLAIMS

What is claimed is:

1. A method of identifying a toxicologically relevant canine gene comprising the steps of:

(a) obtaining a gene expression profile of untreated canine cells;

(b) obtaining a gene expression profile of canine cells treated with an agent; and

(c) comparing the gene expression profile of untreated canine cell with the gene expression profile of the treated canine cells to obtain a gene expression profile indicative of a toxicological response.

2. The method according to claim 1 wherein the canine cells are kidney cells.

3. The method according to claim 2 wherein the kidney cells are MDCK cells.

4. The method according to claim 1 wherein the canine cells are isolated from a biological sample.

5. The method according to claim 1 wherein the gene expression profile is obtained by:

(a) providing canine cells;

(b) dividing said cells into two groups;

(c) using the first group of canine cells as a control group;

(d) exposing the second group of canine cells to an agent;

(e) isolating RNA from the first and second groups of canine cells;

(f) generating double stranded cDNA from said RNA;

(g) labeling said cDNA;

(h) resolving said cDNA on a gel; and

(i) comparing intensity of bands between the group of cells or tissue exposed to said agent and the group of cells or tissue not exposed to said agent.

6. The method according to claim 5 wherein the gene expression profile is stored in a database.

7. The method according to claim 1 wherein the gene expression profile is obtained by transcriptome profiling.

8. The method according to claim 1 wherein said agent is an agent listed in Table 10.

9. A method of isolating canine genes indicative of a toxicological response to an agent comprising the steps of:

(a) providing sequences of mammalian non-canine genes associated with toxicological responses;

(b) providing primers homologous to said genes; and

(c) using said primers to amplify canine genes from a canine cDNA library.

10. The method according to claim 9 wherein the mammalian non-canine gene is a human gene.

11. The method according to claim 9 wherein the mammalian non-canine gene is a rat gene.

12. A method for determining a toxicological response to an agent comprising the steps of:

(a) exposing cells to an agent;

(b) obtaining a first gene expression profile from said cells;

(c) comparing the first gene expression profile with a gene expression profile of toxicologically relevant canine genes; and

(d) determining if the first gene expression profile is indicative of a toxicological response.

13. The method according to claim 12 wherein at least one gene expression profile of a toxicologically relevant canine gene is stored in a database.

14. The method according to claim 12 wherein said toxicological response is selected from the group consisting of a cellular response, pathological change, and histological change.

15. A method for determining a toxicological response in an organ to an agent comprising the steps (a) - (c) according to claim 12 and further comprising an additional step of determining if the first gene expression profile is indicative of a toxicological response in an organ.

16. The method according to claim 15 wherein said toxicological response is a change in physiological function of the organ.

17. A method for screening an agent for a potential toxicological response comprising the steps of:

(a) exposing cells to an agent;

(b) obtaining a first gene expression profile from said cells;

(c) comparing the first gene expression profile with a gene expression profile of toxicologically relevant canine genes to determine if the first gene expression profile is indicative of a toxicological response in genes associated with toxic responses.

18. The method according to claim 17 wherein at least one gene expression profile of a toxicologically relevant canine gene is stored in a database.

19. The method according to claim 17 wherein said agent is a drug.

20. The method according to claim 17 wherein said agent is a pharmaceutical composition.

21. A method for generating a canine array comprising isolating at least ten canine genes which are indicative of a toxicological response and attaching said genes to a substrate.

22. The method according to claim 21 wherein said substrate is a solid substrate.

23. The method according to claim 22 wherein said solid substrate comprises glass.

24. An array comprising of at least ten canine toxicological response genes or a portion thereof immobilized on a substrate.

25. The array according to claim 24 wherein said substrate is a solid substrate.

26. The array according to claim 25 wherein said solid substrate comprises glass.

27. The array according to claim 24 wherein said genes are attached to said substrate by covalent linkage.

28. The array according to claim 24 wherein said genes or portions thereof are capable of hybridization to expressed nucleic acids derived from a cell and are capable of indicating a toxic response of the cell to said agent.

29. The array according to claim 24 wherein said genes have a gene expression indicative of toxicological response to an agent listed in Table 10.

30. The array according to claim 24 comprising at least 10 canine toxicological genes or a portion thereof.

31. The array according to claim 24 comprising at least 25 canine toxicological genes or a portion thereof.

32. The array according to claim 24 comprising at least 50 canine toxicological genes or a portion thereof.

33. The array according to claim 24 comprising at least 100 canine toxicological genes or a portion thereof.

34. The array according to claim 24 comprising at least 250 canine toxicological genes or a portion thereof.

35. The array according to claim 24 comprising at least 500 canine toxicological genes or a portion thereof.

36. The array according to claim 24 comprising at least 750 canine toxicological genes or a portion thereof.

37. The array according to claim 24 comprising at least 1000 canine toxicological genes or a portion thereof.

38. An array comprising at least 10 genes of Table 8.

39. An array comprising at least 10 genes of Table 9.

40. A method for obtaining a gene expression profile comprising exposing a population of cells to an agent, obtaining cDNA from said population of cells, labeling said cDNA, and contacting said cDNA with the array according to claim 20.